

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/637,302C

DATE: 08/22/2002
TIME: 16:34:07

Input Set : A:\TSRI7102Seq-list.TXT
Output Set: N:\CRF3\08222002\1637302C.raw

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<110> APPLICANT: HOOD, John
                                                                ENTERED
  5
          ELICEIRI, Brian
  6
          CHERESH, David
    <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
          MODULATION OF ANGIOGENESIS USING TYROSINE KINASE RAF AND RAS
 12 <130> FILE REFERENCE: TSRI 710.2
 14 <140> CURRENT APPLICATION NUMBER: US 09/637,302C
 15 <141> CURRENT FILING DATE: 2000-08-11
 17 <150> PRIOR APPLICATION NUMBER: US 60/148,924
 18 <151> PRIOR FILING DATE: 1999-08-13
 20 <150> PRIOR APPLICATION NUMBER: US 60/215,951
 21 <151> PRIOR FILING DATE: 2000-07-05
 23 <160> NUMBER OF SEQ ID NOS: 7
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 27 <210> SEQ ID NO: 1
28 <211> LENGTH: 2977
 29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (130)...(2073)
36 <400> SEQUENCE: 1
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39 gctgcatca atg gag cac ata cag gga gct tgg aag acg atc agc aat ggt 171
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             Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly
41
43 ttt gga ttc aaa gat gcc gtg ttt gat ggc tcc agc tgc atc tct cct
                                                                      219
44 Phe Gly Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro
45 15
                         20
47 aca ata gtt cag cag ttt ggc tat cag cgc cgg gca tca gat gat ggc
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48 Thr Ile Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly
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51 aaa ctc aca gat cct tct aag aca agc aac act atc cgt gtt ttc ttg
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52 Lys Leu Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu
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55 ccg aac aag caa aga aca gtg gtc aat gtg cga aat gga atg agc ttg
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56 Pro Asn Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu
57
                                70
59 cat gac tgc ctt atg aaa gca ctc aag gtg agg ggc ctg caa cca gag
                                                                      411
60 His Asp Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu
                            85
                                                90
63 tgc tgt gca gtg ttc aga ctt ctc cac gaa cac aaa ggt aaa aaa gca
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9.0	Arg	Leu	Asp	Trp	Asn	Thr	Asp	Ala	Ala	Ser	Leu	Ile	Gly	Ğlu	Ğlu	Leu	
65					115					120					125		
71	caa	gta	gat	ttc	ctg	gat	cat	gtt	ccc	ctc	aca	aca	cac	aac	ttt	gct	555
73	Gln	vaı	Asp	Pne	Leu	Asp	His	Val		Leu	Thr	Thr	His	Asn	Phe	Ala	
		ааσ	aoo	130	at a	226	~++		135					140			
76	cgg Arg	Lvs	Thr	Phe	Len	Luc	Lou	gcc Ala	Dho	cur	gac	atc	tgt	cag	aaa	ttc	603
77	5	-1-	145		LCu	Lys	пец	150	rne	Cys	ASP	116	155	GIN	ьуs	Phe	
79	ctg	ctc	aat	qqa	ttt	cga	t.at.		act	tat	aac	tac	TOO	+++	oa+	a 2 a	651
80	Leu	Leu	Asn	Ğĺy	Phe	Arg	Cys	Gln	Thr	Cvs	Glv	Tvr	Lvs	Phe	His	Glu	651
9.1		TPO					165					170					
83	cac	tgt	agc	acc	aaa	gta	cct	act	atg	tgt	gtg	gac	tgg	aqt	aac	atc	699
84	HIS	Cys	Ser	Thr	Lys	Val	Pro	Thr	Met	Cys	Val	Asp	Trp	Ser	Asn	Ile	
85	175					180					185					190	
0 / Q Q	aga	Cla	CTC	tta	ttg	ttt	cca	aat	tcc	act	att	ggt	gat	agt	gga	gtc	747
89	Arg	GIII	ьeu	Leu	ьеи 195	Pne	Pro	Asn	Ser		Ile	Gly	Asp	Ser		Val	
	cca	αca	cta	cct		t t a	201	2+4	aa+	200	a+-				205	_	
92	Pro	Ala	Leu	Pro	Ser	Leu	Thr	Mot	Ara	Ara	alg Mot	Cga Ara	gag	Com	gtt	tcc	795
93				210	-	Dea	1111	MCC	215	AIY	Met	Arg	GIU	220	vaı	ser	
95	agg	atg	cct	gtt	agt	tct	caq	cac		tat	tct	aca	cct	CAC	acc	ttc	843
96	Arg	Met	Pro	Val	Ser	Ser	Gln	His	Arg	Tyr	Ser	Thr	Pro	His	Ala	Phe	043
97			225						-	-							
			225					230					235				
99	acc	ttt	aac	acc	tcc	agt	ccc	tca	tct	gaa	ggt	tcc	ct.c	tcc	cag	agg	891
100	Thr	Phe	aac Asn	acc Thr	tcc Ser	agt Ser	Pro	tca	tct Ser	gaa Glu	ggt Gly	tcc Ser	ct.c	tcc Ser	cag Gln	agg Arg	891
10	) Thr L	240	aac Asn	Thr	Ser	Ser	Pro 245	tca Ser	Ser	Glu	Gly	Ser 250	ctc Leu	Ser	Gln	Arg	891
100 100 100	Thr L B cag	Phe 240 agg	aac Asn tcg	Thr	ser tcc	Ser aca	Pro 245 cct	tca Ser aat	Ser gtc	Glu	Gly	Ser 250 gtc	ctc Leu	Ser	Gln	Arg	891 939
100 100 100 100	Thr l G cag	240 agg Arg	aac Asn tcg	Thr	ser tcc	Ser aca Thr	Pro 245 cct	tca Ser aat	Ser gtc	Glu	Gly atg Met	Ser 250 gtc Val	ctc Leu	Ser	Gln	Arg ctg Leu	
10: 10: 10: 10:	l Cag Gln 255	240 agg Arg	aac Asn tcg Ser	aca Thr	tcc Ser	s Ser aca Thr 260	Pro 245 cct Pro	tca Ser aat Asn	Ser gtc Val	Glu cac His	Gly atg Met 265	Ser 250 gtc Val	ctc Leu agc Ser	Ser acc Thr	Gln acg Thr	ctg Leu	939
100 100 100 100 100	Thr cag Gln 255	240 agg Arg	aac Asn tcg Ser gac	aca Thr	tcc Ser	aca Thr 260	Pro 245 cct Pro att	tca Ser aat Asn	gtc Val	Glu cac His	atg Met 265	Ser 250 gtc Val	ctc Leu agc Ser	Ser acc Thr	Gln acg Thr	ctg Leu 270	
100 100 100 100 100 100 100	Cag Gln G255 Cct Pro	240 agg Arg gtg Val	aac Asn tcg Ser gac Asp	aca Thr agc Ser	tcc Ser agg Arg 275	aca Thr 260 atg	Pro 245 cct Pro att Ile	tca Ser aat Asn gag Glu	gtc Val gat Asp	cac His gca Ala 280	atg Met 265 att Ile	Ser 250 gtc Val cga Arg	ctc Leu agc Ser agt Ser	acc Thr cac	acg Thr agc Ser	ctg Leu 270 gaa Glu	939
100 100 100 100 100 100 100 100 110	Cag Gln 255 Cct Pro	240 agg Arg gtg Val	aac Asn tcg Ser gac Asp	Thr aca Thr agc Ser	tcc Ser agg Arg 275	aca Thr 260 atg Met	Pro 245 cct Pro att Ile	tca Ser aat Asn gag Glu	gtc Val gat Asp	cac His gca Ala 280	atg Met 265 att Ile	Ser 250 gtc Val cga Arg	ctc Leu agc Ser agt Ser	Ser acc Thr cac His	Gln acg Thr agc Ser 285	ctg Leu 270 gaa Glu	939 987
100 103 104 105 107 108 109 111	Cag Cag Cag Cag Cag Cag Cag Cag Cag Cag	240 agg Arg gtg Val	aac Asn tcg Ser gac Asp	Thr aca Thr agc Ser cct Pro	tcc Ser agg Arg 275	aca Thr 260 atg Met	Pro 245 cct Pro att Ile	tca Ser aat Asn gag Glu	gtc Val gat Asp	cac His gca Ala 280	atg Met 265 att Ile	Ser 250 gtc Val cga Arg	ctc Leu agc Ser agt Ser	Ser acc Thr cac His	Gln acg Thr agc Ser 285	ctg Leu 270 gaa Glu	939
100 103 104 105 107 108 109 113 112 113	Glanding Control Contr	gtg Val	tcg Ser gac Asp tca Ser	aca Thr agc Ser cct Pro	tcc Ser agg Arg 275 tca Ser	aca Thr 260 atg Met gcc Ala	Pro 245 cct Pro att Ile ctg Leu	tca Ser aat Asn gag Glu tcc Ser	gtc Val gat Asp agt Ser 295	cac His gca Ala 280 agc Ser	atg Met 265 att Ile ccc Pro	Ser 250 gtc Val cga Arg aac Asn	ctc Leu agc Ser agt Ser aat Asn	ser acc Thr cac His ctg Leu 300	acg Thr agc Ser 285 agc Ser	ctg Leu 270 gaa Glu cca Pro	939 987
100 103 103 103 103 108 109 113 113 115	3 cag 3 Gln 5 255 7 cct 3 Pro 1 tca 5 Ser	gtg yal gcc Ala	aac Asn tcg Ser gac Asp tca Ser	aca Thr agc Ser cct Pro 290	tcc Ser agg Arg 275 tca Ser	aca Thr 260 atg Met gcc Ala	Pro 245 cct Pro att Ile ctg Leu	tca Ser aat Asn gag Glu tcc ser	gtc Val gat Asp agt Ser 295	cac His gca Ala 280 agc Ser	atg Met 265 att Ile ccc Pro	Ser 250 gtc Val cga Arg aac Asn	ctc Leu agc Ser agt Ser aat Asn	acc Thr cac His ctg Leu 300	acg Thr agc Ser 285 agc Ser	ctg Leu 270 gaa Glu cca Pro	939 987
100 101 102 103 103 103 113 113 115	3 cag 3 Gln 5 255 7 cct 3 Pro 5 tca 5 Ser 6 aca Thr	gtg yal gcc Ala	aac Asn tcg Ser gac Asp tca Ser tgg Trp	aca Thr agc Ser cct Pro 290	tcc Ser agg Arg 275 tca Ser	aca Thr 260 atg Met gcc Ala	Pro 245 cct Pro att Ile ctg Leu	tca Ser aat Asn gag Glu tcc Ser acc Thr	gtc Val gat Asp agt Ser 295	cac His gca Ala 280 agc Ser	atg Met 265 att Ile ccc Pro	Ser 250 gtc Val cga Arg aac Asn	ctc Leu agc Ser agt Ser aat Asn caa Gln	acc Thr cac His ctg Leu 300	acg Thr agc Ser 285 agc Ser	ctg Leu 270 gaa Glu cca Pro	939 987 1035
100 101 102 103 103 103 103 113 113 115 116	3 cag 3 Gln 5 255 7 cct 3 Pro 5 tca 5 Ser 6 aca Thr	gtg yal gcc Ala ggc Gly	aac Asn tcg Ser gac Asp tca Ser tgg Trp 305	aca Thr agc Ser cct Pro 290 tca Ser	tcc Ser agg Arg 275 tca Ser cag	aca Thr 260 atg Met gcc Ala	Pro 245 cct Pro att Ile ctg Leu aaa Lys	tca Ser aat Asn gag Glu tcc Ser acc Thr 310	gtc Val gat Asp agt Ser 295 ccc Pro	cac His gca Ala 280 agc Ser gtg Val	atg Met 265 att Ile ccc Pro	Ser 250 gtc Val cga Arg aac Asn gca	ctc Leu agc Ser agt Ser aat Asn caa Gln 315	ser acc Thr cac His ctg Leu 300 aga Arg	acg Thr agc Ser 285 agc Ser gag Glu	ctg Leu 270 gaa Glu cca Pro	939 987 1035 1083
100 103 103 103 103 103 113 113 115 116 117	Gln Cotton Cotto	gtg yal gcc Ala ggc Gly cca	aac Asn tcg Ser gac Asp tca Ser tgg Trp 305 gta	Thr aca Thr agc Ser cct Pro 290 tca Ser tct	tcc Ser agg Arg 275 tca Ser cag Gln	aca Thr 260 atg Met gcc Ala ccg Pro	Pro 245 cct Pro att Ile ctg Leu aaa Lys	tca Ser aat Asn gag Glu tcc Ser acc Thr 310	gtc Val gat Asp agt Ser 295 ccc Pro	cac His gca Ala 280 agc Ser gtg Val	atg Met 265 att Ile ccc Pro	Ser 250 gtc Val cga Arg aac Asn gca Ala	agc Ser agt Ser aat Asn caa Gln 315	Ser acc Thr cac His ctg Leu 300 aga Arg	acg Thr agc Ser 285 agc Ser gag Glu	ctg Leu 270 gaa Glu cca Pro cgg Arg	939 987 1035
100 103 103 103 103 103 113 113 115 116 117	3 cag 3 Gln 5 255 7 cct 6 Pro 5 tca 5 Ser aca Thr gca Ala	gtg yal gcc Ala ggc Gly cca	aac Asn tcg Ser gac Asp tca Ser tgg Trp 305 gta	Thr aca Thr agc Ser cct Pro 290 tca Ser tct	tcc Ser agg Arg 275 tca Ser cag Gln	aca Thr 260 atg Met gcc Ala ccg Pro	Pro 245 cct Pro att Ile ctg Leu aaa Lys cag Gln	tca Ser aat Asn gag Glu tcc Ser acc Thr 310	gtc Val gat Asp agt Ser 295 ccc Pro	cac His gca Ala 280 agc Ser gtg Val	atg Met 265 att Ile ccc Pro	Ser 250 gtc Val cga Arg aac Asn gca Ala att	agc Ser agt Ser aat Asn caa Gln 315	Ser acc Thr cac His ctg Leu 300 aga Arg	acg Thr agc Ser 285 agc Ser gag Glu	ctg Leu 270 gaa Glu cca Pro cgg Arg	939 987 1035 1083
100 103 103 103 103 103 113 113 115 116 117 119 120 121	3 cag 3 Gln 5 255 7 cct 6 Pro 5 tca 5 Ser aca Thr gca Ala	gtg Val gcc Ala ggc Cly cca Pro 320	tcg Ser gac Asp tca Ser tgg Trp 305 gta Val	Thr aca Thr agc Ser cct Pro 290 tca Ser tct Ser	tcc Ser agg Arg 275 tca Ser cag Gln	aca Thr 260 atg Met gcc Ala ccg Pro acc	Pro 245 cct Pro att Ile ctg Leu aaa Lys cag Gln 325	tca Ser aat Asn gag Glu tcc Ser acc Thr 310 gag Glu	gtc Val gat Asp agt Ser 295 ccc Pro aaa Lys	cac His gca Ala 280 agc Ser gtg Val aac Asn	atg Met 265 att Ile ccc Pro cca Pro aaa Lys	Ser 250 gtc Val cga Arg aac Asn gca Ala att Ile 330	agc Ser agt Ser aat Asn caa Gln 315 agg	cac Thr cac His ctg Leu 300 aga Arg	acg Thr agc Ser 285 agc Ser gag Glu cgt	ctg Leu 270 gaa Glu cca Pro cgg Arg	939 987 1035 1083
100 103 103 103 103 103 113 115 116 117 119 120 121 123 124	3 cag 3 cag 5 Cott 6 Pro 1 tca 5 Ser 1 aca Thr Ga Ala Cag Gln	gtg val gcc Ala ggc cca Pro 320 aga	aac Asn tcg Ser gac Asp tca Ser tgg Trp 305 gta Val	Thr aca Thr agc Ser cct Pro 290 tca Ser tct Ser	tcc Ser agg Arg 275 tca Ser cag Gln	aca Thr 260 atg Met gcc Ala ccg Pro acc Thr	Pro 245 cct Pro att Ile ctg Leu aaa Lys cag Gln 325 tat	tca Ser aat Asn gag Glu tcc Ser acc Thr 310 gag Glu tgg	gat yal agt Ser 295 ccc Pro aaa Lys	cac His gca Ala 280 agc Ser gtg Val aac Asn	atg Met 265 att Ile ccc Pro cca Pro aaa Lys	Ser 250 gtc Val cga Arg aac Asn gca Ala att Ile 330 gcc	agc Ser agt Ser aat Asn caa Gln 315 agg Arg	ser acc Thr cac His ctg Leu 300 aga Arg cct Pro	acg Thr agc Ser 285 agc Ser gag Glu cgt Arg	ctg Leu 270 gaa Glu cca Pro cgg Arg	939 987 1035 1083
100 103 103 103 103 103 113 115 116 117 119 120 121 123 124 125	3 cag 3 cag 5 cct 6 Pro 5 tca 5 Ser aca Thr gca Ala cag Gln 335	gtg Val gcc Ala ggc Gly cca Pro 320 aga Arg	tcg Ser gac Asp tca Ser tgg Trp 305 gta Val gat Asp	Thr aca Thr agc Ser cct Pro 290 tca Ser tct Ser tct Ser	tcc Ser agg Arg 275 tca Ser cag Gln ggg Gly agc	ser aca Thr 260 atg Met gcc Ala ccg Pro acc Thr tat Tyr 340	Pro 245 cct Pro att Ile ctg Leu aaa Lys cag Gln 325 tat	tca Ser aat Asn gag Glu tcc Ser acc Thr 310 gag Glu tgg Trp	gat gat Ser 295 CCC Pro aaa Lys gaa Glu	cac His gca Ala 280 agc Ser gtg Val aac Asn	atg Met 265 att Ile ccc Pro cca Pro aaa Lys gaa Glu 345	Ser 250 gtc Val cga Arg aac Asn gca Ala att Ile 330 gcc Ala	agc Ser agt Ser aat Asn caa Gln 315 agg Arg	cac Thr cac His ctg Leu 300 aga Arg cct Pro	acg Thr agc Ser 285 agc Ser gag Glu cgt Arg	ctg Leu 270 gaa Glu cca Pro cgg Arg gga Gly atg Met 350	939 987 1035 1083
100 103 103 103 103 103 113 113 115 116 117 119 120 121 123 124 125 127	Gln cag Gln aca Ala cag Gln 335 ctg	gtg yal gcc Ala ggc Gly cca Arg Arg tcc	tcg Ser gac Asp tca Ser tgg Trp 305 gta Val gat Asp	Thr aca Thr agc Ser cct Pro 290 tca Ser tct Ser tca Ser	tcc Ser agg Arg 275 tca Ser cag Gln ggg Gly agc Ser	ser aca Thr 260 atg Met gcc Ala ccg Pro acc Thr tat Tyr 340 ggg	Pro 245 cct Pro att Ile ctg Leu aaa Lys cag Gln 325 tat Tyr	tca Ser aat Asn gag Glu tcc Ser acc Thr 310 gag Glu tgg Trp	gat Asp agt Ser 295 CCC Pro aaa Lys gaa Glu	cac His gca Ala 280 agc Ser gtg Val aac Asn ata Ile	atg Met 265 att Ile ccc Pro cca Pro aaa Lys gaa Glu 345	Ser 250 gtc Val cga Arg aac Asn gca Ala att Ile 330 gcc Ala	agc Ser agt Ser aat Asn caa Gln 315 agg Arg	ser acc Thr cac His ctg Leu 300 aga Arg cct Pro gaa Glu	acg Thr agc Ser 285 agc Ser gag Glu cgt Arg	ctg Leu 270 gaa Glu cca Pro cgg Arg gga Gly atg Met 350	939 987 1035 1083
100 103 103 103 103 103 113 113 115 116 117 119 120 121 123 124 125 127	3 cag 3 cag 5 Cott 6 Pro 1 tca 5 Ser 1 aca Thr Ga Ala Cag Gln	gtg yal gcc Ala ggc Gly cca Arg Arg tcc	tcg Ser gac Asp tca Ser tgg Trp 305 gta Val gat Asp	Thr aca Thr agc Ser cct Pro 290 tca Ser tct Ser tca Ser	tcc Ser agg Arg 275 tca Ser cag Gln ggg Gly agc Ser	ser aca Thr 260 atg Met gcc Ala ccg Pro acc Thr tat Tyr 340 ggg	Pro 245 cct Pro att Ile ctg Leu aaa Lys cag Gln 325 tat Tyr	tca Ser aat Asn gag Glu tcc Ser acc Thr 310 gag Glu tgg Trp	gat Asp agt Ser 295 CCC Pro aaa Lys gaa Glu	cac His gca Ala 280 agc Ser gtg Val aac Asn ata Ile	atg Met 265 att Ile ccc Pro cca Pro aaa Lys gaa Glu 345	Ser 250 gtc Val cga Arg aac Asn gca Ala att Ile 330 gcc Ala	agc Ser agt Ser aat Asn caa Gln 315 agg Arg	ser acc Thr cac His ctg Leu 300 aga Arg cct Pro gaa Glu	acg Thr agc Ser 285 agc Ser gag Glu cgt Arg	ctg Leu 270 gaa Glu cca Pro cgg Arg gga Gly atg Met 350	939 987 1035 1083 1131 1179

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Output Set: N:\CRF3\08222002\1637302C.raw

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13	2 Lvs	s Tri	o His	Gli	, Agr	. Val	. gcc	Val	i uag	, all	To	1 aay	9 yuu	. g.c	gad	Pro	1275
13.	<i>1</i> -	,		370	)	, , ,	. 1110	· vu.	375		: пе	т груг	o val			Pro	
		e eca	a gad			cao	י מככ	. ++/				· ~+^	. ~~+	380	) +-	g cgc	1200
130	6 Thi	r Pro	o Glu	Glr	Phe	Gln	Δla	Dha	. agg	l aat	yay	y y L	9 900	- gui	CCC	g cgc L Arg	1323
13	7		385	5		. 011	nic	390		HSI	LGI	ı val			. Let	ı Arg	
		a aca			ato	aac	att			++	+.	. ~~	395	) 		aag	1001
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143	 L	400	)	,	, , ,		405		пец	FILE	: Met	410		Met	. Thi	Lys	
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145	5 415	5				420	1111	OII.	ıııp	Суз	425		ser	ser	теп		
			e eta	cat	ato			acc	י אפרי	+++			++-			430 att	1467
148	Lvs	His	Leu	His	Val	Gln	Glii	Thr	· Lug	Dho	Cla	Mot	Dho	Cay	CLd	Ile	1467
149	) 1				435	0111	Olu		шуз	440		ı met	. Pile	GIL	леи 445		
		att	acc	caa			act	cad	тпа			. + = +	++~	aa+	445	aag	1515
152	Asp	Ile	Ala	Ara	Gln	Thr	Ala	Gln	Glv	Mot	yac	Tur	. LLY	Udl	yca	Lys	1515
153	, -			450				011	455		пор	, 1 A T	ьец	460		гЛЯ	
155	aac	ato	atc			gac	atα	aaa			aat	ata	+++	2+0	ast	gaa	1562
156	Asn	Ile	Ile	His	Ara	Asp	Met	Lvs	Ser	Δen	Δen	Tla	Dho	Tou	Uat	Glu	1563
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160	Gly	Leu	Thr	Val	Lvs	Ile	Glv	Asp	Phe	Glv	T.e.ii	Δla	Thr	y ca V = 1	Tuc	Con	1611
161		480			4		485			0-1	LCu	490	1111	Val	цуз	ser	
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164	Arg	Trp	Ser	`Gly	Ser	Gln	Gln	Val	Glu	Gln	Pro	Thr	Glv	Sor	Val	Lou	1039
165	495	_		-		500					505		011	DCL	vul	510	
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168	Trp	Met	Ala	Pro	Ğlu	νaί	Ile	Arq	Met	Gln	Asp	Asn	Asn	Pro	Phe	Ser	1/0/
169					515			_		520					525	DCI	
171	ttc	cag	tcg	gat	gtc	tac	tcc	tat	qqc	atc	gta	t.t.a	tat	αаа	cta	ato	1755
172	Phe	Gln	Ser	Asp	Val	Tyr	Ser	Tyr	Gly	Ile	Val	Leu	Tvr	Glu	Leu	Met	1733
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183	aag	aac	tgc	ccc	aaa	gca	atg	aag	agg	ctg	gta	gct	qac	tqt	ata	aaσ	1899
184	ьуs	Asn	Cys	Pro	Lys	Ala	Met	Lys	Arg	Leu	Val	Āla	Asp	Cys	Val	Lvs	
182	3/5					580					585					590	
187	aaa	gta	aag	gaa	gag	agg	cct	ctt	ttt	ccc	cag	atc	ctq	tct	tcc	att	1947
188	Lys	Val	Lys	Glu	Glu	Arg	Pro	Leu	Phe	Pro	Gln	Ile	Leu	Ser	Ser	Ile	
189					595					600					605		
191	gag	ctg	ctc	caa	cac	tct	cta	ccg	aag	atc	aac	cgg	agc	gct	tcc	gag	1995
192	Glu	Leu	Leu	GIn	His	Ser	Leu	Pro	Lys	Ile	Asn	Arg	Ser	Ala	Ser	Glu	
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Input Set : A:\TSRI7102Seq-list.TXT
Output Set: N:\CRF3\08222002\1637302C.raw

195 cca tcc ttg cat cgg gca gcc cac act gag gat atc aat gct tgc acg 2043 196 Pro Ser Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr 630 199 ctg acc acg tcc ccg agg ctg cct gtc ttc tagttgactt tgcacctgtc 2093 200 Leu Thr Thr Ser Pro Arg Leu Pro Val Phe 640 645 203 ttcaggctgc caggggagga ggagaagcca gcaggcacca cttttctgct ccctttctcc 2153 204 agaggcagaa cacatgtttt cagagaagct ctgctaagga ccttctagac tgctcacagg 2213 205 gccttaactt catgttgcct tcttttctat ccctttgggc cctgggagaa ggaagccatt 2273 206 tgcagtgctg gtgtgtcctg ctccctcccc acattcccca tgctcaaggc ccagccttct 2333 207 gtagatgcgc aagtggatgt tgatggtagt acaaaaagca ggggcccagc cccagctgtt 2393 208 ggctacatga gtatttagag gaagtaaggt agcaggcagt ccagccctga tgtggagaca 2453 209 catgggattt tggaaatcag cttctggagg aatgcatgtc acaggcggga ctttcttcag 2513 210 agagtggtgc agcgccagac attttgcaca taaggcacca aacagcccag gactgccgag 2573 211 actctggccg cccgaaggag cctgctttgg tactatggaa cttttcttag gggacacgtc 2633 212 ctcctttcac agettctaag gtgtccagtg cattgggatg gttttccagg caaggcactc 2693 213 ggccaatccg catctcagcc ctctcaggag cagtcttcca tcatgctgaa ttttgtcttc 2753 214 caggagetge ecetatgggg egggeegeag ggeeageetg tttetetaac aaacaaacaa 2813 215 acaaacagcc ttgtttctct agtcacatca tgtgtataca aggaagccag gaatacaggt 2873 216 tttcttgatg atttgggttt taattttgtt tttattgcac ctgacaaaat acagttatct 2933 217 gatggtccct caattatgtt attttaataa aataaattaa attt 219 <210> SEQ ID NO: 2 220 <211> LENGTH: 648 221 <212> TYPE: PRT 222 <213> ORGANISM: Homo sapiens 224 <400> SEQUENCE: 2 225 Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly Phe Gly 226 1 5 227 Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro Thr Ile 228 229 Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly Lys Leu 230 231 Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu Pro Asn 232 233 Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu His Asp 70 235 Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys 236 237 Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala Arg Leu 238 100 105 239 Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu Gln Val 115 120 241 Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala Arg Lys 135 243 Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe Leu Leu 244 145 155 245 Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu His Cys 165 170 247 Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile Arg Gln

Input Set : A:\TSRI7102Seq-list.TXT
Output Set: N:\CRF3\08222002\I637302C.raw

240																
248		_		180					185					190		
		Leu			Pro	Asn	Ser			Gly	Asp	Ser	Gly	Val	Pro	Ala
250			195					200					205			
251	Leu			Leu	Thr	Met			Met	Arg	Glu	Ser	Val	Ser	Arg	Met
252		210					215					220				
253	Pro	Val	Ser	Ser	Gln	His	Arg	Tyr	Ser	Thr	Pro	His	Ala	Phe	Thr	Phe
254	225					230					235					240
255	Asn	Thr	Ser	Ser	Pro	Ser	Ser	Glu	Gly	Ser	Leu	Ser	Gln	Arg	Gln	Arg
256					245					250				_	255	
257	Ser	Thr	Ser	Thr	Pro	Asn	Val	His	Met	Val	Ser	Thr	Thr	Leu	Pro	Val
258				260					265					270		
259	Asp	Ser	Arg	Met	Ile	Glu	Asp	Ala	Ile	Arq	Ser	His	Ser	Glu	Ser	Ala
260			275				_	280		_			285			
261	Ser	Pro	Ser	Ala	Leu	Ser	Ser	Ser	Pro	Asn	Asn	Leu	Ser	Pro	Thr	Gly
262		290					295					300				1
263	Trp	Ser	Gln	Pro	Lys	Thr	Pro	Val	Pro	Ala	Gln	Ara	Glu	Ara	Ala	Pro
	305				-	310					315	,		5		320
265	Val	Ser	Gly	Thr	Gln	Glu	Lvs	Asn	Lvs	Ile		Pro	Ara	Glv	Gln	Arg
266			_		325		-		_	330			5	1	335	9
267	Asp	Ser	Ser	Tyr	Tyr	Trp	Glu	Ile	Glu	Ala	Ser	Glu	Va 1	Met		Ser
268	-			340	•	-			345					350		001
269	Thr	Arg	Ile	Gly	Ser	Gly	Ser	Phe	Glv	Thr	Val	Tvr	Lvs	Glv	Lvs	Trp
270		_	355	•		-		360				-1-	365	1	~15	
271	His	Gly	Asp	Val	Ala	Val	Lvs	Ile	Leu	Lvs	Va1	Val		Pro	Thr	Pro
272		370	_				375			4		380				
273	Glu	Gln	Phe	Gln	Ala	Phe	Ara	Asn	Glu	Va 1	Ala		Len	Arσ	T.vs	Thr
274	385					390					395			5		400
275	Arq	His	Val	Asn	Ile		Leu	Phe	Met	Glv		Met	Thr	T.vs	Δsn	
276	_				405					410	-1-			_1_	415	
277	Leu	Ala	Ile	Val	Thr	Gln	Trp	Cys	Glu		Ser	Ser	Leu	Tvr		His
278				420			-	_	425	1				430	-10	
279	Leu	His	Val	Gln	Glu	Thr	Lvs	Phe	Gln	Met	Phe	Gln	Leu		Asp	Tle
280			435				•	440					445			
281	Ala	Arq	Gln	Thr	Ala	Gln	Glv	Met	Asp	Tvr	Leu	His	Ala	Lvs	Asn	Tle
282		450					455		•	- 4		460		-1-		
283	Ile	His	Arg	Asp	Met	Lys	Ser	Asn	Asn	Ile	Phe		His	Glu	Glv	Len
284			-	•		470					475				0-1	480
285	Thr	Val	Lys	Ile	Gly	Asp	Phe	Gly	Leu	Ala		Va l	Lvs	Ser	Ara	
286			-		485	•		-		490			-1-		495	
287	Ser	Gly	Ser	Gln	Gln	Val	Glu	Gln	Pro	Thr	Glv	Ser	Va l	Leu	Tro	Met
288		_		500					505		1			510		
289	Ala	Pro	Glu	Val	Ile	Arq	Met	Gln		Asn	Asn	Pro	Phe		Phe	G1n
290			515					520	E				525			0111
291	Ser	Asp		Tyr	Ser	Tvr	Glv	Ile	Val	Leu	Tvr	Glu		Met	Thr	Glv
292		530					535				-1-	540			~ ***	J_1
	Glu	Leu	Pro	Tyr	Ser	His	Ile	Asn	Asn	Arσ	Asp		Ile	Ile	Phe	Met
294	545		_	<b>4</b> -		550				3	555	··				560
		Gly	Arq	Glv			Ser	Pro	Asp	Len		Lvs	Leu	Tvr	Lvs	
296		-	-	-	565				F	570		-, 0		-1-	575	
										٠. ٠					J , J	

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/637,302C
DATE: 08/22/2002
TIME: 16:34:08

Input Set : A:\TSRI7102Seq-list.TXT
Output Set: N:\CRF3\08222002\1637302C.raw

L:412 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5 L:415 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5 L:533 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:536 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6